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1645

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/987,107

DATE: 02/12/2002

TIME: 15:32:09

Input Set : A:\GRAVERSEN1A.txt

Output Set: N:\CRF3\02122002\I987107.raw

ENTERED

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3 <110> APPLICANT: GRAVERSEN, Jonas
4      MOESTRUP, Soren
6 <120> TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
8 <130> FILE REFERENCE: GRAVERSEN1A
10 <140> CURRENT APPLICATION NUMBER: US 09/987,107
11 <141> CURRENT FILING DATE: 2001-11-13
13 <150> PRIOR APPLICATION NUMBER: US 60/264,022
14 <151> PRIOR FILING DATE: 2001-01-26
16 <150> PRIOR APPLICATION NUMBER: DK PA2001 00057
17 <151> PRIOR FILING DATE: 2001-01-15
19 <150> PRIOR APPLICATION NUMBER: DK PA2000 01682
20 <151> PRIOR FILING DATE: 2000-11-10
22 <160> NUMBER OF SEQ ID NOS: 91
24 <170> SOFTWARE: PatentIn version 3.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 243
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
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37 Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln
38      20      25      30
41 Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Asp
42      35      40      45
45 Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu
46      50      55      60
49 Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu
50      65      70      75      80
53 Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys
54      85      90      95
57 Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met
58      100     105     110
61 Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu
62      115     120     125
65 Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu
66      130     135     140
69 Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg
70      145     150     155     160
73 Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala
74      165     170     175
77 Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr
78      180     185     190

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81 His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys
82 195 200 205
85 Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser
86 210 215 220
89 Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu
90 225 230 235 240
93 Asn Thr Gln
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 244
99 <212> TYPE: PRT
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104 <222> LOCATION: (1)..(1)
105 <223> OTHER INFORMATION: N-terminal Cys
108 <220> FEATURE:
109 <221> NAME/KEY: misc_feature
110 <222> LOCATION: (2)..(244)
111 <223> OTHER INFORMATION: Amino acids 25-267 from human ApoA1
114 <400> SEQUENCE: 2
116 Cys Asp Glu Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala
117 1 5 10 15
120 Thr Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser
121 20 25 30
124 Gln Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu
125 35 40 45
128 Asp Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln
129 50 55 60
132 Leu Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr
133 65 70 75 80
136 Glu Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala
137 85 90 95
140 Lys Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu
141 100 105 110
144 Met Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln
145 115 120 125
148 Gln Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro
149 130 135 140
152 Leu Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu
153 145 150 155 160
156 Arg Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala
157 165 170 175
160 Ala Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu
161 180 185 190
164 Tyr His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala
165 195 200 205
168 Lys Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu
169 210 215 220
172 Ser Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys

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Input Set : A:\GRAVERSENIA.txt
 Output Set: N:\CRF3\02122002\I987107.raw

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181 <211> LENGTH: 301
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183 <213> ORGANISM: Homo sapiens
185 <220> FEATURE:
186 <221> NAME/KEY: misc_feature
187 <222> LOCATION: (1)..(58)
188 <223> OTHER INFORMATION: Trimerisation module from tetranectin
191 <220> FEATURE:
192 <221> NAME/KEY: misc_feature
193 <222> LOCATION: (59)..(301)
194 <223> OTHER INFORMATION: Mature ApoA1
197 <400> SEQUENCE: 3
199 Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn
200 1                      5                      10                      15
203 Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
204                      20                      25                      30
207 Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
208                      35                      40                      45
211 Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Asp Glu Pro Pro Gln Ser
212                      50                      55                      60
215 Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu
216 65                      70                      75                      80
219 Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu
220                      85                      90                      95
223 Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr
224                      100                      105                      110
227 Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu
228                      115                      120                      125
231 Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met
232                      130                      135                      140
235 Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp
236 145                      150                      155                      160
239 Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys
240                      165                      170                      175
243 Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu
244                      180                      185                      190
247 His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp
248                      195                      200                      205
251 Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr
252                      210                      215                      220
255 Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg Leu Glu Ala Leu Lys
256 225                      230                      235                      240
259 Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His Ala Lys Ala Thr Glu
260                      245                      250                      255
263 His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro Ala Leu Glu Asp Leu
264                      260                      265                      270

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267 Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe Lys Val Ser Phe Leu
268          275          280          285
271 Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn Thr Gln
272          290          295          300
275 <210> SEQ ID NO: 4
276 <211> LENGTH: 258
277 <212> TYPE: PRT
278 <213> ORGANISM: Homo sapiens
280 <220> FEATURE:
281 <221> NAME/KEY: misc_feature
282 <222> LOCATION: (1)..(58)
283 <223> OTHER INFORMATION: Trimerisation module from tetranectin
286 <220> FEATURE:
287 <221> NAME/KEY: misc_feature
288 <222> LOCATION: (59)..(258)
289 <223> OTHER INFORMATION: Amion acids 68-267 from human Apo Al
292 <400> SEQUENCE: 4
294 Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn
295 1          5          10          15
298 Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
299          20          25          30
302 Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
303          35          40          45
306 Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Leu Lys Leu Leu Asp Asn
307          50          55          60
310 Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly
311 65          70          75          80
314 Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly
315          85          90          95
318 Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Val Lys Ala Lys Val
319          100         105         110
322 Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu
323          115         120         125
326 Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly
327          130         135         140
330 Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly
331 145         150         155         160
334 Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr
335          165         170         175
338 His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala Arg
339          180         185         190
342 Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr His
343          195         200         205
346 Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys Pro
347          210         215         220
350 Ala Leu Glu Asp Ser Arg Gln Gly Leu Leu Pro Val Leu Glu Ser Phe
351 225         230         235         240
354 Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu Asn
355          245         250         255

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358 Thr Gln
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363 <211> LENGTH: 301
364 <212> TYPE: PRT
365 <213> ORGANISM: Homo sapiens
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369 <222> LOCATION: (1)..(58)
370 <223> OTHER INFORMATION: Trimerisation module from tetranectin
373 <220> FEATURE:
374 <221> NAME/KEY: misc_feature
375 <222> LOCATION: (9)..(9)
376 <223> OTHER INFORMATION: Mutagen
379 <220> FEATURE:
380 <221> NAME/KEY: misc_feature
381 <222> LOCATION: (15)..(15)
382 <223> OTHER INFORMATION: Mutagen
385 <220> FEATURE:
386 <221> NAME/KEY: misc_feature
387 <222> LOCATION: (59)..(301)
388 <223> OTHER INFORMATION: Apo-A1 mature
391 <400> SEQUENCE: 5
393 Ser Pro Gly Thr Glu Pro Pro Thr Gln Lys Pro Lys Ala Ile Val Asn
394 1 5 10 15
397 Ala Lys Ala Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser
398 20 25 30
401 Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln
402 35 40 45
405 Ala Leu Gln Thr Val Ser Leu Lys Gly Ser Asp Glu Pro Pro Gln Ser
406 50 55 60
409 Pro Trp Asp Arg Val Lys Asp Leu Ala Thr Val Tyr Val Asp Val Leu
410 65 70 75 80
413 Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln Phe Glu Gly Ser Ala Leu
414 85 90 95
417 Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp Asn Trp Asp Ser Val Thr
418 100 105 110
421 Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu Gly Pro Val Thr Gln Glu
422 115 120 125
425 Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu Gly Leu Arg Gln Glu Met
426 130 135 140
429 Ser Lys Asp Leu Glu Glu Val Lys Ala Lys Val Gln Pro Tyr Leu Asp
430 145 150 155 160
433 Asp Phe Gln Lys Lys Trp Gln Glu Glu Met Glu Leu Tyr Arg Gln Lys
434 165 170 175
437 Val Glu Pro Leu Arg Ala Glu Leu Gln Glu Gly Ala Arg Gln Lys Leu
438 180 185 190
441 His Glu Leu Gln Glu Lys Leu Ser Pro Leu Gly Glu Glu Met Arg Asp
442 195 200 205
445 Arg Ala Arg Ala His Val Asp Ala Leu Arg Thr His Leu Ala Pro Tyr

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